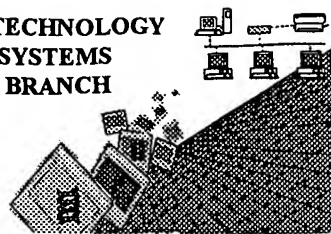


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/020,436
Source: OIPE
Date Processed by STIC: 2/21/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/020,436

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping"
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ✓ Variable Length Sequence(s) 1-2,4 contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIFE

RAW SEQUENCE LISTING

DATE: 02/21/2002

PATENT APPLICATION: US/10/020,436

TIME: 11:29:58

Input Set : A:\39200.app

Output Set: N:\CRF3\02212002\J020436.raw

3 <110> APPLICANT: PEPTIDE THERAPEUTICS LIMITED et al
 5 <120> TITLE OF INVENTION: A METHOD FOR MAPPING THE ACTIVE SITES BOUND BY ENZYMES
 6 THAT COVALENTLY MODIFY SUBSTRATE MOLECULES
 8 <130> FILE REFERENCE: 39200A/JMD/NT
 10 <140> CURRENT APPLICATION NUMBER: US/10/020,436
 11 <141> CURRENT FILING DATE: 2001-12-18
 13 <150> PRIOR APPLICATION NUMBER: GB 9722818.3
 14 <151> PRIOR FILING DATE: 1997-10-30
 16 <160> NUMBER OF SEQ ID NOS: 21
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 3
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Artificial Sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Description of Artificial Sequence: formula for a
 27 library comprising natural and/or unnatural amino
 28 acid residues or peptidomimetics
 30 <220> FEATURE:
 31 <221> NAME/KEY: UNSURE
 32 <222> LOCATION: (1)
 33 <223> OTHER INFORMATION: Xaa at position 1 is any natural or unnatural
 34 amino acid residue or peptidomimetic and is
 35 repeated x times
 37 <220> FEATURE:
 38 <221> NAME/KEY: UNSURE
 39 <222> LOCATION: (2)
 40 <223> OTHER INFORMATION: Xaa at position 2 is a non-degenerate modifiable
 41 natural or unnatural amino acid residue or
 42 peptidomimetic
 44 <220> FEATURE:
 45 <221> NAME/KEY: UNSURE
 46 <222> LOCATION: (3)
 47 <223> OTHER INFORMATION: Xaa at position 3 is any natural or unnatural
 48 amino acid residue or peptidomimetic and is
 49 repeated y times.
 51 <220> FEATURE:
 52 <221> NAME/KEY: UNSURE
 53 <222> LOCATION: (1)..(3)
 54 <223> OTHER INFORMATION: x and y are each independently 0 or an integer; (x
 55 + y) = (n - 1); and n = an integer from 3 to 8,
 56 preferably 5
 58 <400> SEQUENCE: 1

Does Not Comply
Corrected Diskette Needed

pp 1-3

invalid - see item 5 on
Erra Summary Sheet

same error
↓

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/020,436

DATE: 02/21/2002
TIME: 11:29:58

Input Set : A:\39200.app
Output Set : N:\CRF3\02212002\J020436.raw

W--> 59 Xaa Xaa Xaa
60 1
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 3
65 <212> TYPE: PRT
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: Description of Artificial Sequence: formula for
70 library used to identify protein kinase inhibitor
71 molecules
73 <220> FEATURE:
74 <221> NAME/KEY: UNSURE
75 <222> LOCATION: (1)
76 <223> OTHER INFORMATION: Xaa at position 1 is any natural or unnatural
77 amino acid residue or peptidomimetic and is
78 repeated x times *item 5*
80 <220> FEATURE:
81 <221> NAME/KEY: UNSURE
82 <222> LOCATION: (3)
83 <223> OTHER INFORMATION: Xaa at position 3 is any natural or unnatural
84 amino acid residue or peptidomimetic and is
85 repeated y times *item 5*
87 <220> FEATURE:
88 <221> NAME/KEY: UNSURE
89 <222> LOCATION: (1)..(3)
90 <223> OTHER INFORMATION: x and y are each independently 0 or an integer; (x
91 + y) = (n-1); and n = an integer from 3 to 8,
92 preferably 5
94 <400> SEQUENCE: 2
W--> 95 Xaa Tyr Xaa
96 1
99 <210> SEQ ID NO: 3
100 <211> LENGTH: 8
101 <212> TYPE: PRT
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus
106 peptide substrate for ZAP-70
108 <220> FEATURE:
109 <221> NAME/KEY: UNSURE
110 <222> LOCATION: (1)
111 <223> OTHER INFORMATION: Biotin-epsilon-amino-hexanoic acid is linked to the
112 aspartic acid residue at position 1
114 <220> FEATURE:
115 <221> NAME/KEY: UNSURE
116 <222> LOCATION: (8)
117 <223> OTHER INFORMATION: Leucine at position 8 is Norleucine
119 <400> SEQUENCE: 3
120 Asp Glu Glu Asp Tyr Phe Glu Leu

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/020,436

DATE: 02/21/2002

TIME: 11:29:58

Input Set : A:\39200.app

Output Set: N:\CRF3\02212002\J020436.raw

```

121      1          5
124 <210> SEQ ID NO: 4
125 <211> LENGTH: 3
126 <212> TYPE: PRT
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: general
131      formula for peptide library containing substrates
132      for protein serine or serine/threonine kinase
133      enzyme
135 <220> FEATURE:
136 <221> NAME/KEY: UNSURE
137 <222> LOCATION: (1)
138 <223> OTHER INFORMATION: Xaa at position 1 is any natural or unnatural
139      amino acid residue or peptidomimetic and is
140      repeated x times
142 <220> FEATURE:
143 <221> NAME/KEY: UNSURE
144 <222> LOCATION: (3)
145 <223> OTHER INFORMATION: Xaa at position 3 is any natural or unnatural
146      amino acid residue or peptidomimetic and is
147      repeated y times
149 <220> FEATURE:
150 <221> NAME/KEY: UNSURE
151 <222> LOCATION: (1)..(3)
152 <223> OTHER INFORMATION: x and y are each independently 0 or an integer; (x
153      + y) = (n - 1); and n = an integer from 3 to 8,
154      preferably 5
156 <400> SEQUENCE: 4
W--> 157 Xaa Ser Xaa
158      1
161 <210> SEQ ID NO: 5
162 <211> LENGTH: 36
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
168      used to amplify the coding sequence for human
169      ZAP-70 amino acids 306-615 from Jurkat T cell cDNA
171 <400> SEQUENCE: 5
172 ccgggatccg ccatgcccat ggacacgagc gtgtat
174 <210> SEQ ID NO: 6
175 <211> LENGTH: 57
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
181      used to amplify the coding sequence for human
182      ZAP-70 amino acids 306-615 from Jurkat T cell cDNA

```

item 5

item 5

36

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/020,436

DATE: 02/21/2002

TIME: 11:29:58

Input Set : A:\39200.app

Output Set: N:\CRF3\02212002\J020436.raw

```

184 <400> SEQUENCE: 6
185 gggggatcct cagtgggtggt ggtgggtggtg ggcacaggca gcctcagcct tctgtgt      57
187 <210> SEQ ID NO: 7
188 <211> LENGTH: 5
189 <212> TYPE: PRT
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Description of Artificial Sequence: sequence of
194     phosphorylated motif identified by screen of
195     library peptides
197 <400> SEQUENCE: 7
198 Asp Glu Glu Asp Tyr
199   1           5
202 <210> SEQ ID NO: 8
203 <211> LENGTH: 5
204 <212> TYPE: PRT
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Description of Artificial Sequence: sequence of
209     phosphorylated motif identified by screen of
210     library peptides
212 <400> SEQUENCE: 8
213 Asp Glu Glu Tyr Phe
214   1           5
217 <210> SEQ ID NO: 9
218 <211> LENGTH: 5
219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Description of Artificial Sequence: sequence of
224     phosphorylated peptide motif identified by screen
225     of library peptides
227 <400> SEQUENCE: 9
228 Asp Glu Tyr Glu Phe
229   1           5
232 <210> SEQ ID NO: 10
233 <211> LENGTH: 5
234 <212> TYPE: PRT
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <221> NAME/KEY: UNSURE
239 <222> LOCATION: (5)
240 <223> OTHER INFORMATION: Leucine at position 5 is Norleucine
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Description of Artificial Sequence: sequence of
244     phosphorylated motif identified by screen of
245     library peptides
247 <400> SEQUENCE: 10
248 Asp Tyr Phe Glu Leu

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/020,436

DATE: 02/21/2002

TIME: 11:29:58

Input Set : A:\39200.app

Output Set: N:\CRF3\02212002\J020436.raw

249 1 5
252 <210> SEQ ID NO: 11
253 <211> LENGTH: 5
254 <212> TYPE: PRT
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide
259 identified as a preferred substrate for Syk
261 <400> SEQUENCE: 11
262 Asp Glu Glu Asp Tyr
263 1 5
266 <210> SEQ ID NO: 12
267 <211> LENGTH: 5
268 <212> TYPE: PRT
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide
273 identified as a preferred substrate for Syk
275 <400> SEQUENCE: 12
276 Asp Glu Glu Tyr Asp
277 1 5
280 <210> SEQ ID NO: 13
281 <211> LENGTH: 5
282 <212> TYPE: PRT
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide
287 identified as a preferred substrate for Syk
289 <400> SEQUENCE: 13
290 Asp Glu Tyr Glu Asp
291 1 5
294 <210> SEQ ID NO: 14
295 <211> LENGTH: 5
296 <212> TYPE: PRT
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide
301 identified as a preferred substrate for Syk
303 <400> SEQUENCE: 14
304 Asp Tyr Glu Glu Val
305 1 5
308 <210> SEQ ID NO: 15
309 <211> LENGTH: 5
310 <212> TYPE: PRT
311 <213> ORGANISM: Artificial Sequence
313 <220> FEATURE:
314 <221> NAME/KEY: UNSURE
315 <222> LOCATION: (5)
316 <223> OTHER INFORMATION: Leucine at position 5 is Norleucine

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/020,436

DATE: 02/21/2002

TIME: 11:29:59

Input Set : A:\39200.app

Output Set: N:\CRF3\02212002\J020436.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4